(Linear) MAP of: Eclga.Seq check: 379 from: 1 to: 2241
Sequence of BCLGA (Green) clones from BaF3 library

	GAATTCGGCACGAGCTCCCTCCTCCTTCCTTCCTTCCTTC	6
1	CTTA ACCUSTOTICAGGGGAGGAGGAGGAAGGAAGGAAGGAAGGAAGGAAGAA	

CCTCCCTCCCTCCCAGTCCTCCACCAGGAAACAACCGGATTCCGGATCCCGGCTGC
61 -----+ 120
GGAGGGAGGGAGGGTCAGGAGGTGGTCCTTTGTTGGCCTAAGGCCTAGGGCCGACG

GGCCTGACCCGGCTCCACTCTAGCCGGGAGGATGAAAGGCCTCAGCTGGGGGCTCCCTGC

		180
121	CCGGACTGGGCCGAGGTGAGATCGGCCCTCCTACTTTCCGGAGTCGACCCCCGAGGGACG	
	CCGCYC.I.gCGCCGYGG.I.C.	

	CACCAGCACTGGGTCCTAAGAGCTGCCATCCAGGCTGGCCGCCCGGATGGCGACCCCAGC	240
181	GTGGTCGTGACCCAGGATTCTCGACGGTAGGTCCGACCGGCGGCCTACCGCTGGGGTCG	

CTCCCTGACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	
CTCAACCCCAGACACACGGGCTCTAGTGGCTGACTTTGTAGGCTATAAGCTGAGGCAGAA	300
 GAGTTGGGGTCTGTGTCCCGAGATCACCGACTGAAACATCCGATATTCGACTCCGTCTT	

CCCAATACAGACACCTCGACCGGGACCCCTTCCGGGTCGGCGGCGGCGGCGACGTGGTTCG

	CATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACCTTCTCTGACCTGGC	
	CATGCGGGCTGCTGGAGACGAGT TGAGAGAG	420
361	CATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACGTTTCGGCAAGAGACTGGACCG	
	CONCCCCGACGACCTCTGCTCAAACTCTGGGC222100	

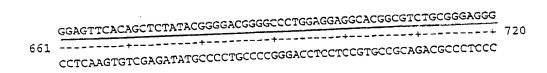
	TO COCCACO ACCOTTCACCCAGGTTTCCGACGA	
	CGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACCCAGGTTTCCGACGA	4\$0
	-ttttttt	
421	GCGAGTCGATGTGCACTGGGGTCCGAGTCGGGTCGTTGCGAAGTGGGTCCAAAGGCTGCT	
	GCGAGTCGATGTGCAC 166662 2001	

ACTTTCCAAGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTTGTCTTTGGGGCTGC

481 ----+ 540
TGAAAAGGTTCCCCCGGGATTGACCCCGGCAGAACACCGTAAGAAACAGAAACCCCGACG

	CCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCTTTGGTGGGACAAGTGCAGATTG	
	CCTGTGTGCTGAGAGIGICAACAY	600
- 41	CCTGTGTGCTGAGAGTGTCAACAAAGAATTGGTGCTGAAC	
34 T		

	GATGGTGGCCTACCTGGAGACACGTCTGGCTGACTGGATCCACAGCAGTGGGGCTGGGC	550
90T	TO SO OFFICATE ACCITITE GENERAL CONTROL OF THE SOURCE ACCITIC TO THE SOURCE ACCITICATE A	



	GAACTGGGCATCAGTGAGGACAGTGCTGACGGGGCCCTGGCACTGGGGCCCTGGTAAC	780
721	GAACTGGGCATCAGTGAGGACAGTGCTGACGACTGCCCCCGGGCACCGTGACCCCCGGGACCATTG	

-

	TGTAGGGGCCTTTTTTGCTAGCAAGTGAGAAAGTCTAGGGCCAGGTGGGGCTAGGTGTGG	840	
781	ACATECOCEC A A A A A COATCOTTCACTCTTCAGATCCCGGTCCACCCCGATCCACACCC		

	CTAGGGGCCAGGAGAGCTGGAACAATAGCGAATGCCCTTGGAAGAAACTGGATGTCACGG	900
841	CAMPERCECTETETERACCTTGTTATCGCTTACGGGAACCTTCTTTGACCTACAGTGCC	

	AACAGAGAAAAGGCAGGGGAAGGTAGTGTGTGTGGGAGCCCATCATCCCAGGCAGG	960
901	AACAGAGAAAGGCAGGGAAGGTAGTGTGTGTGTGTGTGTG	

		GGGAGAATGAGTTGGAAACATTAAGGAATGTTTCAAGGCCTAGAACCCAGAGAGTGGAGT	1020
	961	GGGAGAATGAGTTGGAAACATTAAGGAATGTTCCAAGGCCTACATCTCACCTCACCTCA	•

CATCCCACGGCTTGGGGGGTGGGGGTGGGGAGGTGGATGAATCATCGCCGGGGGGGG	

	CACACAACTACCCGGAACATGGCTTGTAGCTCCCAAGGACGGTGAGCTTACTTCANAGAT	
	CACACAACTACCCGGGATCTTTTTTTTTTTTTTTTTTTT	1140
1081	CACACACTACCCGGAACATGGCTTGTACCGAACATCGAGGGTTCCTGCCACTCGAATGAAGTNTCTA	
	THE THE THE SECOND THE TACCE AREA CATCE AGG GTTCCTGCCAC TO GAA TO AND THE TACCE AGG GTTCCTGCCAC TO GAA TO G	

CTGTGTCTCGACTAGATGAATGGGATTTAGGAGCCTAGAATTCACTTCCCTTTGGGATGG+ GACACAGAGCTGATCTACCTTAACCCTAAATCCTCGGATCTTAAGTGAAGGGAAACCCTACC	

;

1261	TGTGCATGTATGTGCACATGCAAGCATGCTCATGTGCATGCTGGGCTGTCTGT	
		1320
	ACACGTACATACACGTGTACGTTCGTACGAGTACACGTACGACCCGACAGACA	
	Achedine	

	GGTGGTGGGGTACTTAGAGAAAACATTCCTTCTTGCTATGGCAAGAACAAGGGGCAGTTC	1200
1321		.בא פרד.
	CCACCACCCATGAATCTCTTTTGTAAGGAAGAACGATACCGTTCTTGTTCCCCGTCAAG	

	ACTGCATCTAGACTAGGGCTCTGGTGCTGCCGAGAGTTGTTGGCAGGGCTTGGGAGAGAA	1500
1441	ACTGCATCTAGACTAGGGCTCTGGTGCTGCCGAGAOTTGTGATCTAGACTAGA	
1501	GAGTTCTGCAGGTGGCCTTGTTCTTCATCATCCCCCTGTGGTGTGCATCTGTGCACCTGG	
7201	CTCAAGACGTCCACCGGAACAAGAAGTAGTAGGGGGACACCACACGTAGACACGTGGACC	
•		
		_
156	GCTGAAAAAGGGTAAAGCTGTGGAGCCTGGGTAGAAGCTTGGGTAGGTGGGACTT	
120	1	C
	GCTGTCACCTCCCAACGGGGGG	 -+ 1680
16	21	

CGACAGTGGAGGGAGG110CCCCCC	
•	
•	
•	
200000	
	ACCAGGG
	+ 1740
1681+	THE CHECCE
1681	1001000
	•
	GCTGAGTA
CCTTTCTTTAGAGCCATATAGTTCCCTTGGGATTAGCTCTTGCCCAAGAAG	+ 1800
1741	CGACTCAT
GGAAAGAAATCTCGGTATATCAAGGGAACCC IAATCGAGIA	
D	

TTCAGATACTAAGTAGCTGGAGAGGATGTTCTTGCTCTCCCAAAGCCCCAAAGGGACAAAT 1861 -----+ 1920 AAGTCTATGATTCATCGACCTCTCCTACAAGAACGAGAGGGTTTCGGGTTTCCCTGTTTA ${\tt AGGGACTTTGCTTAGGCCAAGGCAAGAGCGCAAGTGGGCACTCAGTCCTGCAGTTACCAG}$ TCCCTGAAACGAATCCGGTTCCGTTCTCGCGTTCACCCGTGAGTCAGGACGTCAATGGTC TCCTACTCCCCACTTACACTAGGGCATACATATACTATTTTACTTTTTTAAATCATAACG 1981 ------ 2040

AGGATGAGGGGTGAATGTGATCCCGTATGTATATGATAAAATGAAAAAATTTAGTATTGC

GCAGGAGAACAGATTTGGTTAGTTTAGAAGAAAAGGAAAACCTCTATAAATATAAATATA 2041 -----+ 2100 CGTCCTCTTGTCTAAACCAATCAAATCTTCTTTTCCTTTTGGAGATATTTATATTTATAT TATTCCTGTATTTTATTTAATAATTTATAAATGCCAAGTTCATTTGACTTTTATTTTTG 2101 -----+ 2160 ATAAGGACATAAAATAAATTATTAAATATTTACGGTTCAAGTAAACTGAAAATAAAAAC TGTAATATGTAATGGTCGTATTAAAAATAAATAAATAAAGCCCAGAAATTTAATGAGGAA 2161 -----+ 2220 ACATTATACATTACCAGCATAATTTTATTTATTTATTTTCGGGTCTTTAAATTACTCCTT

AAAAAAAAAAAAACTCGAG
2221 ----+- 2241
TTTTTTTTTTTTTTGAGCTC